1) ygbB
atgcgaattggacacggttttgacgtacatgcctttggcggtgaaggcccaattatcattggtggcgtacgcattccttacgaaaa
aggattgctggcgcattctgatggcgacgtggcgctccatgcgttgaccgatgcattgcttggcgcggcgggcgctggggggatat
cggcaagctgttcccggataccgatccggcatttaaaggtgccgatagcccgagctgctacgcgaaagcctggcgctgattc
aggcgaagggttataccccttggcaacgtcgatgtcactatcatcgctcaggcaccgaagatgttgccgcacattccacaaatg
cgcgtgtttattgccgaagatctcggctgccatatggatgatgttaacgtgaaagccactactacggaaaaactgggattaccg
gacgtggggaagggattgcctgtgaagcggtggcgctactcattaaggcaacaaaatga (SEQ ID NO: 16)

2) yfhC
atgcgccgcgcttttataaccggagttttcttttgtctgaagtcgaatttagccacgaatactggatgcgtcacgcgctgacgctg
gcgaaacgtgcctgggatgagcgggaaggtgccggtcggcgcggtattagtgcataacaatcgggtaatcggcgaaggctg
gaaccgcccgattggtcgccatgatcccaccgcacatgcagaaatcatggccctgcggcagggtggtctggtgatgcaaaat
tatcgtctgatcgacgccacgttgtatgtcacgcttgaaccatgtgtaatgtgtgcccggagcgatgatccacagtcgcattggtcg
cgtggtctttggtgcgcgtgacgcgaaaactggcgctgcgggatcttaatggatgtgctgcatcatccgggtatgaatcaccga
gtggaaattacggaaggaatactggccggatgagtgcgcggccgttgctcagtgacttctttcgcatgcgccgccaggaaattaa
agcgcagaaaaaagcgcaatcctccgacggattaa (SEQ ID NO: 17)

3) yacE
atgaggtatatagttgccttaacgggaggcattggcagtggcaagagtaccgttgccaatgcgtttgctgatctcggaattaacg
tcattgatgccgatattattgcgcgtcaggtggttgaaccaggtgcacctgcgctacatgccattgctgatcactttggcgctaaca
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attgctggtagaaaactcactgtataaaaaagcgaatcgagtgcttgtgggatgttcagcccagaaacgcaacttaagcgc
accatgcagcgcgatgatgtaactcgcgagcatgtcgaacaaatccttgctgctcaggcaacgcgcgaagcccgccttgccg
tggcagatgacgtcattgataataaccggcgcaccggatgctatcggcatcggatgttgcccgcctgcacgcacactatttgcagc
ttgcgtcgcagtttgtctcacaggaaaaaccgtaa (SEQ ID NO: 18)

4) ychB
atgcggacacagtggccctctccggcaaaacttaatctgttttttatacattaccggtcagcgtgcggatggttaccacacgctgc
aaacgctgtttcagttttcttgattacggcgacaccatcagcattgagcttcgtgacgatggggatattcgtctgttaacgcccgttg
aaggcgtggaacatgaagataacctgatcgttcgcgagcgcgattgttgatgaaaactgcggcagacagcgggcgtcttcc
gacgggaagcggtgcgaatatcagcattgacaagcgtttgccgaaggcgttggtgaaatactaacgccggtggatccgccagaga
agtggtatctggtggcgcaccctggtgtaagtattccgactccggtgattttaaagatcctgaactcccgcgcaatacgccaaa
aaggtcaatagaaacgtttcgtctgctaaaatgtgaattcagcaatgtggcgaggttatcgcaagaaaacgttttcgcgaggttgagtgc
ggtgctttcctggctgttagaataacgccccgtcgcgcctgactggtgacaggggcctgtgtgtcttttgctgaatttgatacagagtctg
aagcccgccaggtgctagagcaagccccggaatggctcaatggctttgtggcgaaaggcgctaatctttccccattgcacag
agccatgctttaa (SEQ ID NO: 19)

5) yejD
atgcgcgacttgataaatttatcgcacagcaactcggcgttagccgtgctattgccgggcgtgaaatccgcggcaatcgtgtcacc
gtcgatggcgaaatccgctaatgcagcgttcaaactgcttcctgaacatgatgtcgcttacgatggcaaccgctggcgcag
caacacggtccacgttacttcatgctcaataagcctcagggctatgtttgctccacggacgaccctgatcacccaacggtgctct
attttcttgatgaaccggtagcgtggaaactgcatcgcggcgggggcggttggatattgatacaccggtctggtgctgatgactga
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gacgatacggcagagcaattgctaaaggcgtgcagctgcataacgaaaaagatctcactaagcctgcggtgctggaagtg
attaccccaacgcaggttcgtctgcaccatcagcgaagggcgttatcatcaggtgaaacgcatgttcgccgccgtgggtaacca
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aagaaattgccagctcgtctaa (SEQ ID NO: 20)

6) yrfl

atgattatgccgcaacatgaccaattacatcgctatctgtttgaaaactttgccgtgcgcggcgaactggtaaccgtttcggaaa
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aacaataaccagcagatgcgcggtgtggcgcgcgtgcagggcgaaattccagaaaatgccgaacctgaaaacgctggtcg
gcaatggttacgtggtgatcaccattacccctgagcgaaggcgaacgctatcagggcgtagttggtctggaaggtgataccctg
gcggcctgcctggaagattactttatgcgttctgaacagctgccgacgcgcctgtttattcgcaccggcgacgtagacggcgaaa
ccggctgcaggcggtatgttgttgcaggtaatgcctgcgcaaaatgcccagcaggacggacttttgaccacctggcgacgctaa
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cggtttacgatccgcaggatgtggagttcaaatgcacctgctcgcgtgaacgttcgccgatgcgctgaaaacgctgcctgatg
aagaagttgatagcatcctggcggaagatggcgaaattgacatgcattgtgattactgcggtaaccactatctgttcaatgcgat
ggatattgctgaaatccgcaacaacgcgtctccggcagatccgcaagttcattaa (SEQ ID NO: 21)

7) yggJ

gtgggggagacgacgcggatttttaactatgcgtatccccccgcatttatcatcctgaaccactgaccagccattctcacatcgcgct
ttgcgaagatgccgccaaccatatcgggcgcgtactgcgcatggggcccgggcaggccgttgcaattgtttgacggtagcaac
caggtctttgacgccgaaattaccagcgccagcaaaaaaagcgtggaagtgaaggtgctggaaggccagatcgacgatcg
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gttgaacgcgtccgcctgctgattggcccggaaggcggtttatcggcagatgaaattgccatgactgccccgctatcaatttactg
atatcctgttgaaagacctcgcgtttgcgtacagagacaactgcgctcaccgccattaccgcgctacaagtacgatttggcgatttg
ggctaa (SEQ ID NO: 22)

8) yjeE

atgatgaatcgagtgaattccgctccctgatgagcaggcaacattagacctgggcgagcgggtagcgaaagcctgcgatggc
gcaaccgtaatctatctgtatggcgatttaggcgcaggtaaaaccaccatttagcccgggaaaaattcaatgatttattgcaggagaacaaaggc
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tcctctgcgggtgaattgttgctggcgcgtttagccggttaa
(SEQ ID NO: 23)

9) yiaO

atgaaattacgctctgtaacctacgcattattcattgctggcctggctgcattcagcacatcttctctggcggcacaatctttacgttt
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gagctgaaattaaaactgttcccggacagcactctcggtaacgcgcaggcgatgatcagccggctacgtggcggccaccatc
gatatggaaatgtccggctcgaataactttgccgggttatcaccagtgatgaactgcttgatgtccctttcctgttccgcgataccg
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cctactggaaaacggctggcgcgatgtcaccaactcgcgcgcaccggttaaaaccccgccgacctgaaagggctgaaa
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24)

10) yrdC

gtgaataataacctgcaaagagacgctatcgcagctgcgatagatgttctcaatgaagaacgtgtcatcgcctatccaacgga
agccgttttcggtgttgggtgcgatcctgatagcgaaacagcagtgatgcgactgttggagttaaaacagcgtccggtgataa
ggggctgatttaatcgcagcaaattacgagcagcttaaacccatattgatgacaccatgttgactgacgtgcagcgtgaaac
cattttttcccgctggccaggtcctgtcacctttgtcttcccgcgcctgcgacaacaccgcgctggttgacgggccgctttgattcg

Fig: 1 continued

cttgctgtacgagtcaccgaccatccgttggtggttgcttgttgtgccaggcttatggtaaaccgctggtttctaccagtgccaacttga
gtggattgccaccttgtcgaacagtagacgaagttcgcgcacaatttggcgcggcgttcccggtgtgcctggtgaaacggggg
gggcgtttaaatccttcagaaatccgcgatgccctgacgggtgaactgtttcgacaggggtaa (SEQ ID NO: 25)

11) yhbC

gtgggcttgtccacattagagcaaaaattaacagagatgattactgcgccagttgaggccctgggtttgaactggttggcatcg
aatttattcgcggtcgcacatccacactgcgcatctatattgatagtgaagatgccatcaatgttgatgattgtgctgatgtgagcc
accaggtaagtgctgtgctggatgttgaagatcccatcaccgttgcttataacctggaagtctcctcaccgggtctcgatcgccc
actgttcacggctgaacactacgcccgttttgtcggagaagaggtgactctggttctccgtatggcggtacaaaaccgtcgtaa
atggcagggcgttatcaaagcggtagacggtgaaatgatcacagttaccgtcgaaggtaaagatgaagtgttcgcgctgagt
aatatccagaaggcgaacctggttccccacttttaa (SEQ ID NO: 26)

12) ygbP

atggcaaccactcatttggatgtttgcgccgtggttccggcggccgatttggccgtcgaatgcaaacggaatgtcctaagcaa
tatctctcaatcggtaatcaaaccattcttgaacactcggtgcatgcgctgctggcgcatccccgggtgaaacgtgtcgtcattgc
cataagtcctggcgatagccgtttttgcacaacttcctctggcgaatcatccgcaaatcaccgttgtagatggcggtgatgagcgt
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ttccctcgtgagctgttacatgactgtctgacgcgcgctctaaatgaaggcgcgactattaccgacgaagcctcgggcgctggaa
tattgcggattccatcctcagttggtcgaaggccgtgcggataacattaaagtcacgcgcccggaagatttggcactggccga
gttttacctcacccgaaccatccatcaggagaatacataa (SEQ ID NO: 27)

13) ybeY

atgagtcaggtgatcctcgatttacaactggcatgtgaagataattccgggttaccggaagagagccagtttcagacatggctg
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tgacctatcgcggtaaggataagccgaccaacgtgctctccttccgtttgaagtgccgcctggcatggaaatgtcgctactgg
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tggtggtgcacggcagtctgcatttgttaggttacgatcacatcgaagatgacgaagcagaagaaatgtgaagccctcgaaac
agagattatgcttgctctgggcctatgaggatccgtacattgccgagaaagaataa (SEQ ID NO: 28)

14) gcpE

atgcataaccaggctccaattcaacgtagaaaatcaacacgtatttacgttgggaatgtgccgattggcgatggtgctcccatc
gccgtacagtccatgaccaatacgcgtacgacagacgtcgaagcaacggtcaatcaaatcaaggcgctggaacgcgttgg
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ctggtggctgacatccacttcgactatcgcattgcgctgaaagtagcggaatacggcgtcgattgtctgcgtattaacctctggca
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atcgctgaaaaagatctgcaagaaaagtatggcgaaccgacgcccgcaggccgttgctggaatctgccatgcgtcatgttgat
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caaaacagatcgatcagccgttgcatctgggatcaccgaagccggtggtgcgcacgggggcagtaaaatccgccattg
gtttaggtctgctgctgtctgaaggcatcggcgacacgtcgcgtatcgctggcggccgatccggtcgaagagatcaaagtc
ggttcgatattttgaaatcgctgcgtatccgttcgcgaggatcaacttcatcgcctgcccgacctgttcgcgtcaggaaattgatg
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caaagaccgtctggacaacaacgatatgatcgaccagctggaagcacgcattcgtgcgaaagccagtcagctggacgaa
gcgcgtcggaattgacgttcagcaggttgaaaaataa
(SEQ ID NO: 29)

15) kdtB

atgcaaaaacgggcgatttatccgggtactttcgatcccattaccaatggtcatatcgatatcgtgacgcgcgccacgcagatgt
tcgatcacgttattctggcgattgccgccagccccagtaaaaaaccgatgtttaccctggaagacgtgtggcactggcacag
caggcaaccgcgcatctggggaacgtggaagtggtcgggtttagtgatttaatggcgaacttcgcccgtaatcaacacgctac
ggtgtcgattcgtggcctgcgtgcggtggcagatttgaatatgaaatgcagctggccgcatatgaatcgccacttaatgccggaa

Fig. 1 continued

ctggaaagtgtgtttctgatgccgtcgaaagagtggtcgtttatctcttcatcgttggtgaaagaggtggcggcgccatcagggcg
atgtcacccatttcctgccggagaatgtccatcaggcgctgatggcgaagttagcgtag (SEQ ID NO: 30)

16) pfs

atgaaaatcggcatcattggtgcaatggaagaagaagttacgctgctgcgtgcacaaaatcgaaaaccgtcaaactatcagtc
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gcgctgggtgccacttttgctgttggaacactgcaagccagatgtgattattaacaccggttctgccggtggcctggcaccaacgt
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cattgctgtagagatggaagcgacggcaatcgcccatgtctgccacaatttcaacgtcccgtttgttgtcgtacgcgccatctcc
gacgtggccgatcaacagtctcatcttagcttcgatgagttcctgcggtgttgccgctaaacagtccagcctgatggttgagtcact
ggtgcagaaacttgcacatggcataa (SEQ ID NO: 31)

17) ycaJ

gtgagcaatctgtcgctcgattttctggataatactttttcaacctctggccgcgcgtatgcggccagaaaatttagcacagtatatc
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ccgccgggtaccggcaaaacaactctcgctgaagtgattgcccgctatgcgaacgctgatgtggaacgtatttctgccgtcac
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cggattatgacgtgccggttcattgcgtaatgcgccgacgaaattaatgaaggaaatgggctacgggcaggaaatatcgttac
gctcatgatgaagcaaacgcttatgctgccggtgaggtttacttcccgcccggaaatagcacaaacacgctattatttcccgaca
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18) b1808

gtgacggacgattttgcaccagacggtcagctggcgaaagcgataccaggctttaagccgcgagaaccacagcgacagat
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gccgcgatttgccaacagtctcaaaggcattgaaatatacgggcaacgtggcgctgctgaaagggcgctcaaactacctctg
cctcgaacgtctcgaacagcaggcgctggcggggggcgatctgccggtacaaatcttaagcgatgtgatcctgctgcgctcct
ggtctaatcaaacagtcgatgtgatatcagcacctgcgtcagcgtgcgggaagattcacagcgtgcgctggtcaccag
caccaacgacaactgtcttggcagcgactgcccgatgtataaagatgtcttgtggtcaaagcacgtaaaaagcgatggac
gccgatgtggtggtggtaaaccatcatcatctctttctggcggatatgcggtggttaaagagagtggattggcgaactgatcccggaag
cggacgtcatgtatcttcgacgaagcccaccagctaccggacattgccagccagtatttggtcagtcactcctccagtcgacaac
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caaattcagcgggcatttttactgctcgatgacaccctggaactttgttatgacgtggcgaaactgtcactggggcgttccgccttg
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aagggcaactgttgcagcaatttgtcagcgcccggtaatgcgcttcttgtggcaaccagcagtttctgggaagggggtggacgtgc
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Fig. 1 continued

tgtcgtttgcgcggtggcgacccgttcgatgaagtgcaactaccagatgccgtcattactctcaaacaggggggtagggcgact
gattcgcgacgccgacgatcgtggcgtgctggtgatttgtgacaatcggctggtgatgcgtccttacggcgcgacgtttctcgcc
agtctgccgcccgcgccacgcacccgtgacattgcccgtgcggttcgtttccttgcgataccatcctccaggtaa (SEQ ID
NO: 33)

19) yeaA

atggctaataaaccttcggcagaagaactgaaaaaaaatttgtccgagatgcagttttacgtgacgcagaatcatgggacag
aaccgccatttacgggtcgtttactgcataacaagcgtgacggcgtatatcactgtttgatctgcgatgcccgctgtttcattccc
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acatggaatgcagcgcatagaaatttcgttgcggtaactgtgatgcccatctggggcatgtcttccccgacgggccgcagccaa
cgggcgaacgttattgtgttaactctgcctctttacgctttaccgatggcgaaaacggcgaagaaatcaacggttga (SEQ
ID NO: 34)

20) yagF

atgaccattgagaaaattttcacccgcaggacgacgcgttttatgcggtgatcacccacgcggcggggccgcagggcgctc
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gctgtgggcggcactgcagtcggtgagcggcggcggcacctggaaaggctgtatttatgacaccgataaaattatcgaggtaatta
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21) b1983

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atgtacaaaagtttatcataacgtcgcaaatctctaa (SEQ ID NO: 36)

22) yidD

atggcgccgccactgtcgcctggctcgcgggtcctgatagccctcattcgggtctatcaacgcctgattagtccgctactcgggc
cgcattgtcgtttcactccaacctgttcaagctacggaattgaggcattgcgcacagtttggagtgataaaaggcagttggttgacg

Fig.   1 continued

gtgaaacgcgtattaaaatgccacccttacaccctggtggtgacgatcccgtcccgcccggaccatttgataccagagaaca
ctaa (SEQ ID NO: 37)

23) yceG
atgaaaaaagtgttattgataatcttgttattgctggtggtactgggtatcgccgctggtgtgggcgtctggaaggttcgccatcttg
ccgacagcaaattgcttatcaaagaagagacgatatttaccctgaagccagggaccggacgtctggcgctcggtgaacagc
tttatgccgataagatcatcaatcgtccacgggttttttcaatggctgctgcgtatcgaaccggatctttctcactttaaagccgggac
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(SEQ ID NO:38)

24) yjbC
atgctgcccgactcatcagtccgtttaaataaatacatcagcgaaagcggaatttgctcacgccgcgaagcggatcgctatatc
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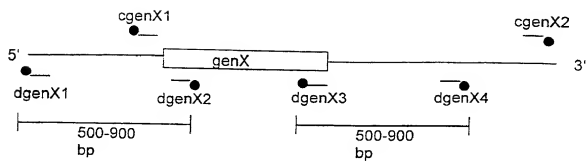aacggtaagcgttttacctcgccggggcgtaaaaagaaggggcgctga (SEQ ID NO:39)

Fig. 1 continued

Fig. 2

E. coli		B. subtilis				H. influenzae			H. pylori		
gene name	GenBank#[1]	gene name	SWItl#[2] or SubtiList#[3]	score	E-value	GenBank#[1]	score	E-value	GenBank#[1]	score	E-value
YqbD	gi17891103	YacN	[2]Q06756	169	2,00E-43	15736372	205	1,00E-54	2314164	105	1,00E-24
Ylbd	gi17189011	Yaal	[2]P21335	135	2,00E-33	15739925	175	1,00E-45	2313814	24	3
YbtG	gi1786292	YtcG	[3]bG13024	135	2,00E-33	15739909	191	2,00E-50	2313965	87	4,00E-19
YtbH	gi17187459	YulaH	[2]P37550	102	3,00E-23	1574450	317	3,00E-88	2314615	41	5,00E-05
YpjD	gi17188510	YtzF	[3]hG13940	126	6,00E-32	1574175	276	2,00E-74	2314637	61	5,00E-11
Yhl	gi17189804	YacC	[2]P37565	71	1,00E-13	15738822	286	5,00E-79	2314407	24	5,4
Yqgal	gi17189315	YqjU	[3]hG12199	96	2,00E-21	15732272	312	1,00E-86	2313478	49	1,00E-07
Ylal	gi17190610	Yobi	[2]hG12199	89	3,00E-19	15730014	171	1,00E-44	2313840	46	9,00E-07
YatO	gi236/210	YdliE	[3]hG12072	148	7,00E-37	15740060	374	1,00E-105	2314105	26	1,5
YutC	gi17189561	YwiC	[2]P39153	93	3,00E-19	15736655	206	3,00E-55	2313122	29	0,13
YulP	gi17189104	YxS	[2]P32726	50	1,00E-19	1574740	157	2,00E-40	2314193	65	1,00E-12
YbuY	gi17186800	YacM	[2]Q06755	129	3,00E-31	15736673	233	4,00E-63	2314164	47	5,00E-07
Gqpl	gi17188063	YqjG	[2]P46347	70	8,00E-14	1572948	190	2,00E-50	2314318	54	3,00E-09
KdlB	gi17190065	YqlY	[2]P54402	310	4,00E-80	15/3337	604	1,00E-174	2313753	294	3,00E-01
pls	gi17186354	Ylbl	[3]hG13561	145	2,00E-36	15736050	176	5,00E-46	2314651	170	3,00E-44
YcaL	gi17187119	YnU	[3]hG13800	244	6,00E-66	1574146	254	2,00E-69	2313168	123	4,00E-30
b1808	gi17188110	YrvN	[3]hG13808	275	5,00E-75	1574435	668	0	2314168	201	3,00E-53
b1808077	gi17188077	binG	[2]P54394	245	6,00E-66	15733557	768	0	2313340	33	0,025
yeaA	gi17186404	YnpQ	[2]P54155	136	2,00E-32	15742293	116	3,00E-28	2313314	125	6,00E-31
ypgl	gi17187185	Ysel	[2]P51785	100	4,00E-46	1573744	168	1,00E-43	2314249	103	2,00E-23
b19ll3	gi17182294	Ysel	[3]hG12H24	279	1,00E-76	15733285	161	2,00E-41	2313249	108	1,00E-25
YbtD	gi140061	YjlA	[3]hG130b5	90	6,00E-19	1176311	96	1,00E-20	2314625	40	8,00E-04

[1] http://www.ncbi.nlm.nih.gov/Entrez/protein.html
[2] http://www.expasy.ch/sprot/
[3] http://www.pasteur.fr/Bio/SubtiList.html
[4] http://www.ncbi.nlm.nih.gov/BLAST/unfinishedgenome.html

Fig. 3

E. coli		M. tuberculosis			Ch. trachomatis			B. burgdorferi		
gene name	GenBank#	GenBank#	score	t-value	GenBank#	score	E-value	GenBank#	score	E-value
YgbU	g1789103	1877312	70	1.00E-16	3320865	62	1.00E-12	2680040	23	4.60E+00
YliiC	g1788911	2960176	119	1.00E-28	3329316	120	2.00E-29	2687969	23	5.20E+00
YmiL	g1788792	2113915	119	1.00E-28	3320928	62	1.00E-11	2680463	41	2.00E-05
YciB	g1787459	2052140	84	1.00E-17	3320270	82	2.00E-17	2680545	23	6.00E+00
Yydu	g1788510	2326754	109	2.00E-25	3329180	105	8.00E-25	2680006	90	5.00E-20
Yiil	g1789804	1550650	25	6.40E+00	3329168	23	7.00E+00	2680577	23	5.40E+00
Ygqi	g1789315	2070027	70	2.00E-13	3320922	23	8.00E+00	2680252	44	4.00E-06
YptE	g1790510	1449365	60	1.00E-10	3320975	61	2.00E-11	2680077	68	1.00E-13
YiaO	g1790004	2113942	27	1.00E+00	3320868	26	1.30E+00	2680570	25	2.70E+00
YdiC	g2367210	1322425	68	8.00E-13	3328537	60	2.00E-13	2680669	73	3.00E-15
YfdC	g1789561	2070017	56	2.00E-09	3328787	26	4.00E-01	2680749	38	1.00E-04
Yqfib	g1789104	1877313	99	3.00E-22	3328906	95	2.00E-21	2680701	26	6.30E-01
YbnY	g1786000	2070032	62	3.00E-11	3328852	26	4.20E-01	2687941	55	6.00E-10
Laql	g1788003	2612813	277	9.00E-76	3328450	155	2.00E-30	2680019	31	5.30E-02
Kdll	g1789005	1694666	140	8.00E-35	3329163	25	9.40E-01	2680262	97	2.00E-22
pfs	g1789354	1405762	100	1.00E-22	3320855	22	6.80E-01	2680200	152	8.00E-39
b1008	g1787719	1460081	329	3.00E-91	3320753	60	1.00E-10	2680379	55	4.00E-09
b1008	g1788110	1340095	274	1.00E-74	3329029	27	9.30E-01	2680551	30	1.30E-01
ysaA	g1788077	1550715	126	8.00E-31	3328854	27	2.20E-01	2680358	23	3.80E+00
ygfl	g1786464	2213526	195	1.00E-50	3329033	28	7.30E-01	2680576	25	4.40E+00
b1983	g1788294	2281051	124	8.00E-30	3320890	118	1.00E-28	2670891	138	1.00E-34
YufD	g1408061	2800707	73	1.00E-13	3320908	56	2.00E-08	2680025	52	3.00E-07

Fig. 3 continued

E. coli gene name	GenBank#	T. pallidum GenBank#	score	E-value	S. pneumoniae contig#	score	E-value	S. aureus contig#	score	E-value
YgbA	g17B9103	3322804	98	1,00E-22	101	n.d.	n.d.	/	n.d.	n.d.
YihC	g17A8911	3322548	33	4,00E-03	17	71	2,00E-12	49	107	2,00E-25
YacE	g17B6292	3322572	36	6,00E-04	/	109	3,00E-24	/	n.d.	n.d.
YchB	g17A7459	3322649	83	7,00E-18	41	n.d.	n.d.	12	n.d.	n.d.
YciD	g17B8510	3322747	97	3,00E-22	7	166	2,00E-41	248	152	5,00E-37
YiiI	g17B9B04	/	n.d.	n.d.	93	80	2,00E-15	90	82	9,00E-16
YggJ	g17A9315	3322550	27	4,50E-01	140	65	1,00E-10	24	86	7,00E-17
YjeI	g17A9G10	3323187	76	6,00E-16	123	80	2,00E-15	/	75	9,00E-14
YacO	g17900G4	3322408	28	2,90E-01	47	n.d.	n.d.	193	n.d.	n.d.
YutC	g2367210	3322447	39	6,00E-05	72	62	9,00E-10	173	76	3,00E-14
YihC	g17B9561	3322709	26	4,40E-01	17	55	8,00E-08	/	90	1,00E-18
YqhP	g17B9104	3322804	58	2,00E-10	232	55	2,00E-07	396	n.d.	n.d.
YhcY	g17G6B80	3322940	40	1,00E-07	156	60	2,00E-09	/	75	7,00E-14
GcpE	g17B0B63	3322731	217	3,00E-58	62	n.d.	n.d.	205	n.d.	n.d.
KdtB	g17900065	3322553	100	2,00E-23	114	113	2,00E-25	1235	149	2,00E-36
pls	g17706354	3322437	112	9,00E-27	31	182	5,00E-06	1085	82	1,00E-15
YcaL	g17B7119	3323329	53	1,00E-00	38	95	2,00E-23	434	150	1,00E-30
b1808	g17B8110	3322379	29	3,50E-01	114	114	5,00E-25	422	34	7,40E-01
yceA	g17B807/	3322932	111	1,00E-26	31	136	2,00E-33	24	112	1,00E-25
yceF	g17B5464	3322975	26	3,20E+00	38	202	1,00E-51	412	171	4,00E-42
b1993	g17A0294	3322762	142	9,00E-36	143	360	1,00E-09	412	163	2,00E-46
YdiD	g1400I61	Treponema g71		4,00E-13	12	64	7,00E-11	1341	76	1,00E-14

Fig. 3 continued

E. coli		E. faecalis*			P. aeruginosa*			B. pertussis*		
gene name	GenBank#	contig#	score	E-value	contig#	score	E-value	contig#	score	E-value
YdjH	g1789103	6177	141	8,00E-34	93	181	5,00E-46	126	139	3,00E-33
YfbC	g1789911	6349	132	3,00E-31	93	151	7,00E-37	737	151	9,00E-37
YaeE	g1786292	6196	111	1,00E-24	95	187	1,00E-47	924	159	3,00E-39
YdhB	g1787459	6342	114	2,00E-25	95	286	2,00E-77	1062	215	9,00E-56
YejD	g1788510	6178	137	2,00E-32	94	198	8,00E-51	983	91	1,00E-18
Yfrl	g1788804	6199	97	2,00E-20	97	192	4,00E-49	1085	160	2,00E-39
YqgJ	g1789315	6207	75	1,00E-13	66	196	4,00E-50	551	119	4,00E-27
Yjtl	g1790610	6204	29	4,00E-00	97	177	7,00E-45	762	125	4,00E-29
YutJ	g1790004	6206	125	1,00E-28	91	139	8,00E-33	459	201	1,00E-51
YtdC	g2367210	6208	96	4,00E-20	75	163	2,00E-40	362	43	4,00E-05
YhhC	g1789561	6465	103	2,00E-22	85	148	6,00E-36	371	76	4,00E-14
YtjP	g1789104	6311	55	2,00E-07	93	180	2,00E-45	126	93	5,00E-19
YbcY	g1786800	6286	67	1,00E-11	91	142	3,00E-34	369	89	5,00E-18
GepE	g1788863	/	n.d.	n.d.	91	514	1,00E-145	862	161	2,00E-39
Kdtll	g1790065	6304	147	1,00E-35	84	197	1,00E-50	1097	172	2,00E-43
pfs	g1786354	6495	201	1,00E-51	/	n.d.	n.d.	/	n.d.	n.d.
b1808	g1787119	6207	138	2,00E-32	89	529	1,00E-150	1043	452	1,00E-127
b1808	g1788110	6205	120	7,00E-27	82	215	1,00E-55	781	255	1,00E-67
yaeA	g1788007 /	6315	130	3,00E-33	81	158	2,00E-39	777	146	1,00E-35
ygjF	g1786464	/	n.d.	n.d.	84	169	1,00E-41	759	160	8,00E-39
b4903	g1788294	6169	309	3,00E-84	82	145	5,00E-35	1059	155	6,00E-38
YsfD	g1408661	/	n.d.	n.d.	46	76	1,00E-14	1007	74	7,00E-14

Fig. 3 continued

E. coli gene name	GenBank#	B. subtilis GenBank#[1]	score	E-value	H. influenzae GenBank#[1]	score	E-value	H. pylori GenBank#[1]	score	E-value
yceG	g1787339	g2635201	140	2e-32	g1073838	289	2e-77	gbAAD07652.1	87	3e-16
yjbC	g396357	g2634751	132	3e-30	g1574128	101	7e-21	g2314637	99	4e-20

E. coli gene name	GenBank#	M. tuberculosis GenBank#[1]	score	E-value	Ch. trachomatis GenBank#[1]	score	E-value	B. burgdorferi GenBank#[1]	score	E-value
yceG	g1787339	embCAB06185	74	2e-12	/	n.d.	n.d.	g2688649	101	1e-20
yjbC	g396357	g2326754	110	1e-23	g3329180	132	2e-30	g2688006	91	1e-17

E. coli gene name	GenBank#	T. pallidum GenBank#[1]	score	E-value	S. pneumoniae* contig#[1]	score	E-value	S. aureus* contig#[1]	score	E-value
yceG	g1787339	g3322780	108	7e-23	/	n.d.	n.d.	/	n.d.	n.d.
yjbC	g396357	g3322747	90	2e-17	12	141	5e-34	4402	134	5e-32

E. coli gene name	GenBank#	E. faecalis* contig#[1]	score	E-value	P. aeruginosa* contig#[1]	score	E-value	B. pertussis* contig#[1]	score	E-value
yceG	g1787339	6216	115	4e-26	54	231	7e-61	398	209	2e-54
yjbC	g396357	6178	118	4e-27	54	109	2e-24	190	123	9e-29

Fig. 3 continued

Multiple sequence alignment of E. coli gene_ygbB with 5 orthologs
from different organisms
Legend: 1 = Escherichia coli; 2 = Haemophilus influenzae;
3 = Bacillus subtilis; 4 = Synechocystis; 5 = Treponema pallidum;
6 = Helicobacter pylori; 7 = Alignment score (* identical :
chemically similar . sterically similar)

```
1  ------------------------------------------------------------
2  ------------------------------------------------------------
3  ------------------------------------------------------------
4  ------------------------------------------------------------
5  MRRGGACVQKKEYLPLTSRQPGVCLLSEILVRALEARSFFLVVVTVPAGEVAYAESQVAC
6  -MSLIRVNGEAFKLSLESLEDPFETKETLETLIKQTSVVLLAAGESRRFSQTIKKQWLR
7
```

```
1  ------------------------------------------------------------
2  ------------------------------------------------------------
3  ------------------------------------------------------------
4  ------------------------------------------------------------
5  DSRLSAFPSRTRPVILYVPGAHTRSASVRAGLDAMATHAPDVVLVHDGARPFVSVALIHS
6  SNHTPLWLSVYESFKEALDFKEIILVVSELDYIYIKRHYPEIKLVKGGASRQESVRNALK
7
```

Fig. 4

```
1  |
2  |
3  |
4  |
5  VLEATCRYGAAVPVIEATDTPKGVAADGSIETHLIRSRVRLAQTPQGFCYASLCAAHHRA
6  IIDSAYTLTSDVARGLANIEALKNLFLTLQQTSHYCIAPYLPCYDTAIYYNEALDREAIK
7  |


1  |
2  |
3  |
4  |
5  ATDGEQYTDDSELYARYG-----GTVHVCAGERSNVKITYPEDLEQRASEPALTRGISVL
6  LIQTPQLSHTKALQSALNQGDFKDESSAILQAFPDRVSYIEGSKDLHKLTTSGDLKHFTL
7  |


1  ------MRIGHGFDVHAFGGEGPIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAA
2  ------MIRIGHGFDVHAFGEDRPLIIGGVEVPYHTGFIAHSDGDVALHALTDAILGAAA
3  -----MFRIGQGFDVHIQLVEGRPLIIGGIEIPYEKGLLGHSDADVLLHTVADACLGAVG
4  ----MTALRIGNGYDIHRLVGDRPLILGGVTIAHHLGLDGHSDADVLTHALMDALLGALS
5  PCTEEGALRVGLGTDMHALCAGRPLILAGIHIPSKKGAQGHSDADVLAHASIDALLGAAG
6  FFNPAKDTFIGMGFDTHAFIKDKPMVLGGVVLDCEFGLKAHSDGDALLHAVIDAILGAIK
7     :* * * *  .: .::  :.*.    .:  *    .   * ***.*.  *:.  *: *  ***
```

```
1 LGDIGKLFPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMR
2 LGDIGKLFPDTDMQYKNADSRGLLREAFRQVQEKGYKIGNVDITIIAQAPKMRPHIDAMR
3 EGDIGKHFPDTDPEFKDADSFKLLQHVWGIVKQKGYVLGNIDCTIIAQKPKMLPYIEDMR
4 LGDIGHYFPPSDARWQGADSLKLLAQVHQLILERGWRINNLDNVIVAEQPKLKPHIQAMK
5 LGDIGTFFPSCDGRWKDAHSCALLRHTWQLVRAACWRLVNLDAVVCLEQPALHPFREAMR
6 GGDIGEWFPDNDPKYKNASSKELLKIVLDFSQSIGFELFEMGATIFSEIPKITPYKPAIL
7 ****  *    ::.*  * *            :   ::   :  :    * :  *: *  .

1 VFIAEDLGCHMDDVNVKATTEKLGFTGREGIACEAVALLIKATK-
2 AKIAEDLQCDIEQVNVKATTEKLGFTGRQEGIACEAVALLIRQ---
3 KRIAEGLEADVSQVNVKATTEKLGFTGRAEGIAAQATVLIQKG---
4 ENLAKVLTIDPDLIGIKATTNERLGPTGREEGIAAYSVALLIKEG--
5 ASLAQALDTHVTRVFVKAKTAERLGPVGSGAAVTAQVVVLLKKI---
6 ENLSQLLGLEKSQISLKATTMEKMGFIGKQEGLLVQAHVSMRYKQKL
7  ::  .    . :**.* *:::* *          .    ::
```